

Sub B1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Ashkenazi, Avi J.
Baker, Kevin
Chuntharapai, Anan
Gurney, Austin
Kim, Kyung Jin
10 Wood, William
- (ii) TITLE OF INVENTION: Apo-2DcR
- (iii) NUMBER OF SEQUENCES: 13
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
20 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 12-Jun-1998
(C) CLASSIFICATION:
- 35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15
Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30
Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35 40 45
His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60
Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

	Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	
					80					85						90
5	Cys	Lys	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	
					95					100						105
	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	
					110					115						120
10	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	
					125					130						135
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	
					140					145						150
15	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	
					155					160						165
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
20					170					175						180
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					185					190						195
25	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					200					205						210
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					215					220						225
30	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	
					230					235						240
	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu	
35					245					250						255

Ile Val Phe Val
259

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50
ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100
CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150
20 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195
Met
1
25 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234
Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
5 10
30 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273
Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
15 20 25
35 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312
Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
35 30 35 40

	CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT	351
	Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys	
	45 50	
5	CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT	390
	Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys	
	55 60 65	
10	AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC	429
	Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser	
	70 75	
15	AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA	468
	Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys	
	80 85 90	
20	TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA	507
	Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg	
	95 100 105	
25	GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT	546
	Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn	
	110 115	
30	GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC	585
	Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys	
	120 125 130	
35	CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG	624
	Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp	
	135 140	
40	GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC	663
	Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala	
	145 150 155	

ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702
 Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
 160 165 170

5 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
 175 180

10 AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
 185 190 195

15 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
 Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
 200 205

20 GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
 210 215 220

GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
 225 230 235

25 GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
 Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
 240 245

30 ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
 250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020

35 AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15
Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30
20
Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
-25 -20 -15
Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5
25
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 15 20
Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30 35
30
Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
40 45 50
Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
35 55 60 65

	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn	
						70				75					80	
5	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp	Gln	
					85					90					95	
	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	Asp	Thr	Val	Cys	Gln	
					100					105					110	
10	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	Glu	Met	Cys	
					115					120					125	
	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn	
					130					135					140	
15	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala	
					145					150					155	
	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
20					160					165					170	
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
					175					180					185	
25	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
					190					195					200	
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
					205					210					215	
30	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
					220					225					230	
	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile	
35					235					240					245	

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTTGACCAG AG ATG CAA GGG GTG AAG GAG 90
Met Gln Gly Val Lys Glu
-40 -35

20 CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

25 CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
-20 -15 -10

30 CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
35 10 15

	CTG	CCA	GTC	CTA	GCT	TAC	TCT	GCC	ACC	ACT	GCC	CGG	CAG	285
	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg	Gln	
		20					25					30		
5	GAG	GAA	GTT	CCC	CAG	CAG	ACA	GTG	GCC	CCA	CAG	CAA	CAG	324
	Glu	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	
				35				40						
	AGG	CAC	AGC	TTC	AAG	GGG	GAG	GAG	TGT	CCA	GCA	GGA	TCT	363
10	Arg	His	Ser	Phe	Lys	Gly	Glu	Glu	Cys	Pro	Ala	Gly	Ser	
	45					50					55			
	CAT	AGA	TCA	GAA	CAT	ACT	GGA	GCC	TGT	AAC	CCG	TGC	ACA	402
	His	Arg	Ser	Glu	His	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	
15				60				65				70		
	GAG	GGT	GTG	GAT	TAC	ACC	AAC	GCT	TCC	AAC	AAT	GAA	CCT	441
	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	
					75					80				
20	TCT	TGC	TTC	CCA	TGT	ACA	GTT	TGT	AAA	TCA	GAT	CAA	AAA	480
	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp	Gln	Lys	
		85					90					95		
25	CAT	AAA	AGT	TCC	TGC	ACC	ATG	ACC	AGA	GAC	ACA	GTG	TGT	519
	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	Asp	Thr	Val	Cys	
				100				105						
	CAG	TGT	AAA	GAA	GGC	ACC	TTC	CGG	AAT	GAA	AAC	TCC	CCA	558
30	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	
	110					115					120			
	GAG	ATG	TGC	CGG	AAG	TGT	AGC	AGG	TGC	CCT	AGT	GGG	GAA	597
	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	
35				125				130				135		

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990

Val Leu Leu Ile Val Phe Val

255

259

5 AAATTCCTTC CTTACCTGAA AGGTTACAGT AGGCGCTGGC TGAGGGCGGG 1040

GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090

AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140

10

. AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15

15 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45

20 Gly Cys Arg Lys
49

25 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

35

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
5 35 40 45

Cys Lys Glu
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1799 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145

Met Glu

1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184

10 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg

5

10

15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala

15

20

25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262

Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val

30

35

40

20

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301

Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala

45

50

25

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340

Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala

55

60

65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379

30

Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu

70

75

80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp

35

85

90

	TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC	457
	Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His	
	95 100 105	
5	TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT	496
	Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys	
	110 115	
10	GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC	535
	Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr	
	120 125 130	
15	AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG	574
	Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg	
	135 140 145	
20	GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA	613
	Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr	
	150 155	
25	GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA	652
	Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr	
	160 165 170	
30	CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC	691
	Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly	
	175 180	
35	ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT	730
	Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile	
	185 190 195	
40	GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA	769
	Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys	
	200 205 210	

	GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT	808
	Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly	
	215	220
5	GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT	847
	Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro	
	225	230 235
10	GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC	886
	Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile	
	240	245
15	TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC	925
	Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val	
	250	255 260
20	CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC	964
	Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser	
	265	270 275
25	CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT	1003
	Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala	
	280	285
30	GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT	1042
	Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn	
	290	295 300
35	GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT	1081
	Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp	
	305	310
40	GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG	1120
	Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro	
	315	320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365

15 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375

20 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390

25 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

30 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
 Ala Asp Ser Ala Xaa Ser
 410 411

CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTTACTGCAC 1550

35 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTT TGGGATGTCA 1650

TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	
					95					100						105
5	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	
					110					115						120
	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	
					125					130						135
10	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro	
					140					145						150
	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
					155					160						165
15	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	
					170					175						180
	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	
20					185					190						195
	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
					200					205						210
25	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	
					215					220						225
	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	
					230					235						240
30	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	
					245					250						255
	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	
35					260					265						270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

Ala Asp Ser Ala Xaa Ser
410 411

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30